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AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions, and listings of claims in the application.

Listing of claims

1. (Currently amended) A method of identifying a human having an altered risk for developing positive autoantibody rheumatoid factor (RF+) Rheumatoid Arthritis (RA), comprising detecting the presence of a single nucleotide polymorphism (SNP) at position 101 of SEQ ID NO: 5502 or its complement thereof in said human's nucleic acids, wherein the presence of the SNP is indicative of an altered risk for developing RF+ RA in said human.

2. - 28. (Canceled)

29. (Currently amended) The method of claim 1 in which SEQ ID NO: 5502 is contained within the genomic sequence of the TRIP gene as ~~represented~~ shown by SEQ ID NO: 1688.

30. (Previously presented) The method of claim 1 in which the SNP to be detected is located at position 6497 of SEQ ID NO: 1688.

31. (Previously presented) The method of claim 1 in which said human's nucleic acids are extracted from a biological sample therefrom.

32. (Currently amended) The method of claim ~~28~~ 31in which said biological sample is blood.

33. (Previously presented) The method of claim 1 in which said human's nucleic acids are amplified before the detection is carried out.

34. (Previously presented) The method of claim 1 in which detection is carried out by using detection reagents comprising the nucleotide sequences of SEQ ID NO: 6629, SEQ ID NO: 6630, and SEQ ID NO: 6631.

35. (Previously presented) The method of claim 1 in which detection is carried out by a process selected from the group consisting of: allele-specific probe hybridization, allele-specific primer extension, allele-specific amplification, sequencing, 5' nuclease digestion, molecular beacon assay, oligonucleotide ligation assay, size analysis, and single-stranded conformation polymorphism.

36. (Currently amended) A method of identifying a human having an increased risk for developing positive autoantibody rheumatoid factor (RF+) Rheumatoid Arthritis (RA), comprising detecting the presence of a single nucleotide polymorphism (SNP) at position 101 of SEQ ID NO: 5502 or its complement thereof in said human's nucleic acids, wherein the presence of ~~the SNP~~ CC at position 101 of SEQ ID NO: 5502 or its complement thereof is indicative of an increased risk for developing RF+ RA in said human.

37. - 38. (Canceled)

39. (Currently amended) The method of claim 36 in which SEQ ID NO: 5502 is contained within the genomic sequence of the TRIP gene as ~~represented~~ shown by SEQ ID NO: 1688.

40. (Previously presented) The method of claim 36 in which the SNP to be detected is located at position 6497 of SEQ ID NO: 1688.

41. (Previously presented) The method of claim 36 in which said human's nucleic acids are extracted from a biological sample therefrom.

42. (Previously presented) The method of claim 41 in which said biological sample is blood.

43. (Previously presented) The method of claim 36 in which said human's nucleic acids are amplified before the detection is carried out.

44. (Previously presented) The method of claim 36 in which detection is carried out by using detection reagents comprising the nucleotide sequences of SEQ ID NO: 6629, SEQ ID NO: 6630, and SEQ ID NO: 6631.

45. (Previously presented) The method of claim 36 in which detection is carried out by a process selected from the group consisting of: allele-specific probe hybridization, allele-specific primer extension, allele-specific amplification, sequencing, 5' nuclease digestion, molecular beacon assay, oligonucleotide ligation assay, size analysis, and single-stranded conformation polymorphism.

46. - 55. (Canceled)

56. (Currently amended) A method of determining a human's risk for developing ~~RA~~ positive autoantibody rheumatoid factor (RF+) Rheumatoid Arthritis (RA), comprising detecting a single nucleotide polymorphism (SNP) at position 101 of SEQ ID NO: 5502 or its complement thereof in said human's nucleic acids, wherein the presence of CC at position 101 of SEQ ID NO: 5502 or its complement thereof is indicative of an increased risk for RF+ RA in said human, or, the presence of T at position 101 of SEQ ID NO: 5502 or its complement thereof is indicative of a decreased risk for developing RF+ RA in said human.

57. - 58. (Canceled)

59. (Currently amended) The method of claim 56 in which SEQ ID NO: 5502 is contained within the genomic sequence of the TRIP gene as ~~represented~~ shown by SEQ ID NO: 1688.

60. (Previously presented) The method of claim 56 in which the SNP to be detected is located at position 6497 of SEQ ID NO: 1688.

61. (Previously presented) The method of claim 56 in which said human's nucleic acids are extracted from a biological sample therefrom.

62. (Previously presented) The method of claim 61 in which said biological sample is blood.

63. (Previously presented) The method of claim 56 in which said human's nucleic acids are amplified before the detection is carried out.

64. (Previously presented) The method of claim 56 in which detection is carried out by using detection reagents comprising the nucleotide sequences of SEQ ID NO: 6629, SEQ ID NO: 6630, and SEQ ID NO: 6631.

65. (Previously presented) The method of claim 56 in which detection is carried out by a process selected from the group consisting of: allele-specific probe hybridization, allele-specific primer extension, allele-specific amplification, sequencing, 5' nuclease digestion, molecular beacon assay, oligonucleotide ligation assay, size analysis, and single-stranded conformation polymorphism.

66. (New) A method of identifying a human having a decreased risk for developing positive autoantibody rheumatoid factor (RF+) Rheumatoid Arthritis (RA), comprising detecting the presence of a single nucleotide polymorphism (SNP) at position 101 of SEQ ID NO: 5502 or its complement thereof in said human's nucleic acids, wherein the presence of T at position 101 of SEQ ID NO: 5502 or its complement thereof is indicative of a decreased risk for RF+ RA in said human.

67. (New) The method of claim 66 in which SEQ ID NO: 5502 is contained within the genomic sequence of the TRIP gene as shown by SEQ ID NO: 1688.

68. (New) The method of claim 66 in which the SNP to be detected is located at position 6497 of SEQ ID NO: 1688.

69. (New) The method of claim 66 in which said human's nucleic acids are extracted from a biological sample therefrom.

70. (New) The method of claim 69 in which said biological sample is blood.

71. (New) The method of claim 66 in which said human's nucleic acids are amplified before the detection is carried out.

72. (New) The method of claim 66 in which detection is carried out by using detection reagents comprising the nucleotide sequences of SEQ ID NO: 6629, SEQ ID NO: 6630, and SEQ ID NO: 6631.

73. (New) The method of claim 66 in which detection is carried out by a process selected from the group consisting of: allele-specific probe hybridization, allele-specific primer extension, allele-specific amplification, sequencing, 5' nuclease digestion, molecular beacon assay, oligonucleotide ligation assay, size analysis, and single-stranded conformation polymorphism.